

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LAL, PREETI
CORLEY, NEIL C.
GUEGLER, KARL J.
PATTERSON, CHANDRA
- (ii) TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: Windows
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Cerrone, Michael C
 - (B) REGISTRATION NUMBER: 39,132
 - (C) REFERENCE/DOCKET NUMBER: PF-0512 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 325 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: THP1AZS08
 - (B) CLONE: 2752518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asp Gly Pro Val Ala Glu His Ala Lys Gln Glu Pro Phe His Val
 1 5 10 15
 Val Thr Pro Leu Leu Glu Ser Trp Ala Leu Ser Gln Val Ala Gly Met
 20 25 30
 Pro Val Phe Leu Lys Cys Glu Asn Val Gln Pro Ser Gly Ser Phe Lys
 35 40 45
 Ile Arg Gly Ile Gly His Phe Cys Gln Glu Met Ala Lys Lys Gly Cys
 50 55 60
 Arg His Leu Val Cys Ser Ser Gly Gly Asn Ala Gly Ile Ala Ala Ala
 65 70 75 80
 Tyr Ala Ala Arg Lys Leu Gly Ile Pro Ala Thr Ile Val Leu Pro Glu
 85 90 95
 Ser Thr Ser Leu Gln Val Val Gln Arg Leu Gln Gly Glu Gly Ala Glu
 100 105 110
 Val Gln Leu Thr Gly Lys Val Trp Asp Glu Ala Asn Leu Arg Ala Gln
 115 120 125
 Glu Leu Ala Lys Arg Asp Gly Trp Glu Asn Val Pro Pro Phe Asp His
 130 135 140
 Pro Leu Ile Trp Lys Gly His Ala Ser Leu Val Gln Glu Leu Lys Ala
 145 150 155 160
 Val Leu Arg Thr Pro Gly Ala Leu Val Leu Ala Val Gly Gly Gly
 165 170 175
 Gly Leu Leu Ala Gly Val Val Ala Gly Leu Leu Glu Val Gly Trp Gln
 180 185 190
 His Val Pro Ile Ile Ala Met His Gly Ala His Cys Phe Asn Ala Ala
 195 200 205
 Ile Thr Ala Gly Lys Leu Val Thr Leu Pro Asp Ile Thr Ser Val Ala
 210 215 220
 Lys Ser Leu Gly Ala Lys Thr Val Ala Ala Arg Ala Leu Glu Cys Met
 225 230 235 240
 Gln Val Cys Lys Ile His Ser Glu Val Val Glu Asp Thr Glu Ala Val
 245 250 255
 Ser Ala Val Gln Gln Leu Leu Asp Asp Glu Arg Met Leu Val Glu Pro
 260 265 270
 Ala Cys Gly Ala Ala Ala Ile Tyr Ser Gly Leu Leu Arg Arg Leu Gln
 275 280 285
 Ala Glu Gly Cys Leu Pro Pro Ser Leu Thr Ser Val Val Val Ile Val
 290 295 300
 Cys Gly Gly Asn Asn Ile Asn Ser Arg Glu Leu Gln Ala Leu Lys Thr
 305 310 315 320
 His Leu Gly Gln Val
 325

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1AZS08
- (B) CLONE: 2752518

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGGTCGACCA CCGTCGCATG ATTAGGATGG TGCATGAGTG ATCGGCAGTG CCCGGGAAAG 60
 CGGTGAGGGT TGCTCTCATC CCCTCTCCTC CTCCGTCTTC ACCCGGAGGC TTAGGGTCTG 120

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GAGCTTTCTC	TTTAACAAAG	GAGGAGGGAC	CAAGGTTGCC	GGAAGCTGCC	TGAAGCTGGA	180
CAGAGCCGGT	TCCTGGAAAG	AGCTGGTTCC	CTGGCAGGCT	GGAGGGCAGG	AGCTGGGGCC	240
ACGCTGGTCT	GGGATAGTTG	GGCAGGGAGG	CTGTCTACCT	GGTCTCCAGA	ATGGACGGCC	300
CTGTGGCAGA	GCATGCCAAG	CAGGAGCCCT	TTCACGTGGT	CACACCTCTG	TTGGAGAGCT	360
GGGCGCTGTC	CCAGGTGGCG	GGCATGCCTG	TCTTCCTCAA	GTGTGAGAAT	GTGCAGCCCA	420
GCGGCTCCTT	CAAGATTCCG	GGCATTGGGC	ATTTCCTGCCA	GGAGATGGCC	AAGAAGGGAT	480
GCAGACACCT	GGTGTGCTCC	TCAGGGGGTA	ATGCGGGCAT	CGCTGCTGCC	TATGCTGCTA	540
GGAAGCTGGG	CATTCTTGCC	ACCATCGTGC	TCCCCGAGAG	CACCTCCCTG	CAGGTGGTGC	600
AGAGGCTGCA	GGGGGAGGGG	GCCGAGGTTT	AGCTGACTGG	AAAGGTCTGG	GACGAGGCCA	660
ATCTGAGGGC	GCAAGAGTTG	GCCAAGAGGG	ACGGCTGGGA	GAATGTCCCC	CCGTTTGACC	720
ACCCCTAAT	ATGGAAAGGC	CACGCCAGCC	TGGTGCAGGA	GCTGAAAGCA	GTGCTGAGGA	780
CCCCACCAGG	TGCCCTGGTG	CTGGCAGTTG	GGGGTGGGGG	TCTCCTGGCC	GGGGTGGTGG	840
CTGGCCTGCT	GGAGGTGGGC	TGGCAGCATG	TACCCATCAT	TGCCATGGAG	ACCCATGGGG	900
CACACTGCTT	CAATGCGGCC	ATCACAGCCG	GCAAGCTGGT	CACACTTCCA	GACATCACCA	960
GTGTGGCCAA	GAGCCTGGGT	GCCAAGACGG	TGGCCGCTCG	GGCCCTGGAG	TGCATGCAGG	1020
TGTGCAAGAT	TCACTCTGAA	GTGGTGGAGG	ACACCGAGGC	TGTGAGCGCT	GTGCAGCAGC	1080
TCCTGGATGA	TGAGCGTATG	CTGGTGGAGC	CTGCCTGTGG	GGCAGCCTTA	GCAGCCATCT	1140
ACTCAGGCCT	CCTGCGGAGG	CTCCAGGCCG	AGGGCTGCCCT	GCCCCCTTCC	CTGACTTCAG	1200
TTGTGGTAAT	CGTGTGTGGA	GGCAACAACA	TCAACAGCCG	AGAGCTGCAG	GCTTTGAAAA	1260
CCCACCTGGG	CCAGGTCTGA	GGGGTCCCAT	CCTGGCCCCA	AAGACCCCTG	AGAGGCCCAT	1320
GGACAGTCCT	GTGTCTGGAT	GAGGAGGACT	CAGTGCTGGC	AGATGGCAGT	GGAAGCTGCC	1380
CTGTGCAACT	GTGCTGGCTG	CCTCCTGAAG	GAAGCCCTCC	TGGACTGCTT	CTTTTGGCTC	1440
TCCGACAACT	CCGGCCAATA	AACACTTTCT	GAATTGAAAA	AAAAA		1485